

APPROVED	O.G. FIG.
BY	CLASS/SUBCLASS
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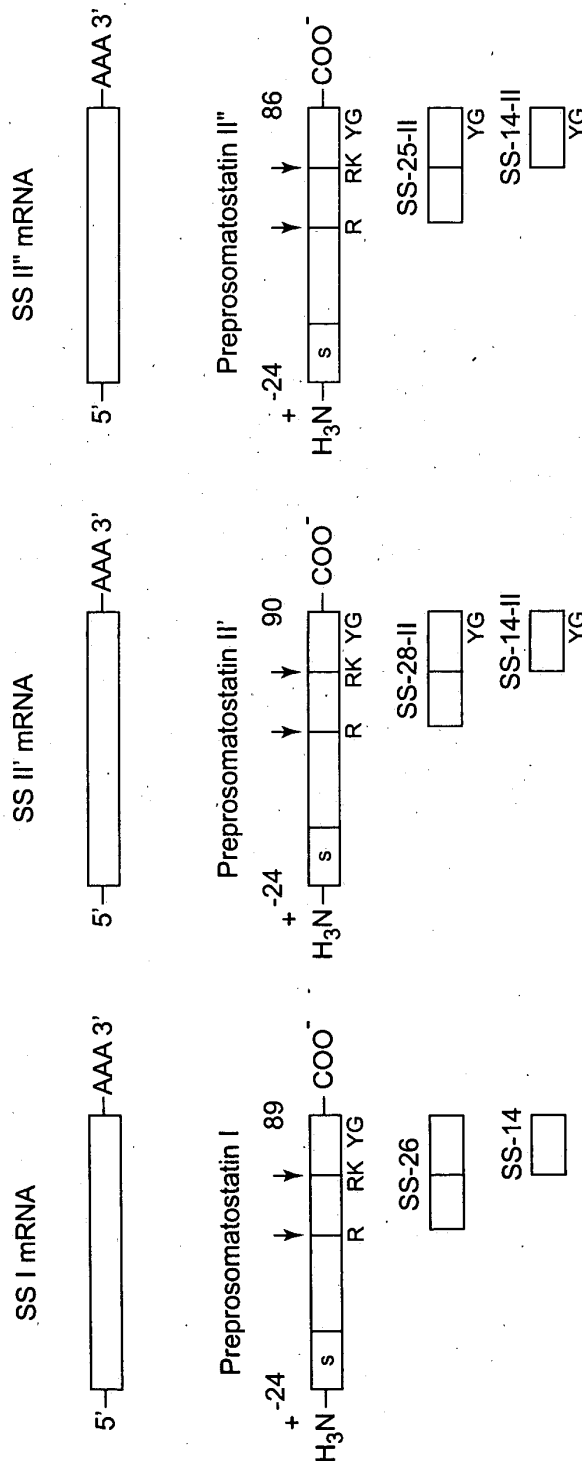


Fig. 1

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P011111 00000000

PPSS-I

SEQ ID NO: 8 5' GGGGGGGGGAACAGGAGCAGCAGAACTCAAGAGAGAGCCCAATCTCAACGATGTCTGCCCAATTGAACCACTTTATCC 81

ATCTCTGCCTCCCCGAGACCCAGAGAAG ATG CTC TCG ACG CGT GTC CAG TGC GCC CTA GCA CTA CTC 152
SEQ ID NO: 3 Met Leu Ser Thr Arg Val Gln Cys Ala Leu Ala Leu Leu -88

TCC CTA GCC CTG GCC ATC AGC AGC GTC TCT GCC GCT CCG TCC GAT GCC AAA CTC CGC CAG CTG 214
Ser Leu Ala Leu Ala Ile Ser Ser Val Ser Ala Ala Pro Ser Asp Ala Lys Leu Arg Gln Leu -67

CTC CAA CGG TCA CTC ATG GCA CCT GCA GGC AAA CAG GAG CTT GCC AGG AAT ACA CTC GTA GAG 272
Leu Gln Arg Ser Leu Met Ala Pro Ala Gly Lys Gln Glu Leu Ala Arg Asn Thr Leu Val Glu -46

CTA CTC TCA GAG CTC GCA CAT GTA GAG AAC GAG GCG ATT GAA TTG GAT GAC ATG TCT CAT GGC 340
Leu Leu Ser Glu Leu Ala His Val Glu Asn Glu Ala Ile Glu Leu Asp Asp Met Ser His Gly -25

GTG GAG CAG GAG GAT GTG GAT CTC GAG CTG GAG CGT GCA CCC GGC CCA GTA CTG GCT CCA CGT 403
Val Glu Gln Glu Asp Val Asp Leu Glu Leu Glu Arg Ala Pro Gly Pro Val Leu Ala Pro Arg -4

GAA CGC AAG GCT GGA TGC AAG AAC TTC TTC TGG AAG ACC TTT ACA TCG TGT TAA TGAATCTACTC 466
Glu Arg Lys Ala Gly Cys Lys Asn Phe Phe Thr Lys Thr Phe Thr Ser Cys ***

CTTTACTGTGTACTACATCTCATCTCTTTTGTTCATCATCTGATGCTGAATCCAATGCACCATGCCCTAACCCCTCTCT 549
TCAAAAAATTTAAATAAACACTGTATATACTTTAAACAATCATCTGATGTTTCTATCGCTCACTTAGATTTTTCGGAAG 632
GAACACAGAAAGAATGTTCTACAAATGATGCGGTCTGCTTTGACTGTGATTTATGATTTTGGCAGACTATTTTAAATTG 715
TTTGTTTGAAATAAAATCTGTGTTTCAGAACCAAAAAA 3'

Fig. 2

Fig. 3

	PPSS-II'	PPSS-II''
	cccgatgatgggtcttgaaatcaacagaatgatgtacctgtctaattgtgaaatāāāatataaaataatg (a) n	cctgatgacaatatgatgattatgatgtacctgactaatttagaaatāāāagagaāatāāāagagaac (a) n

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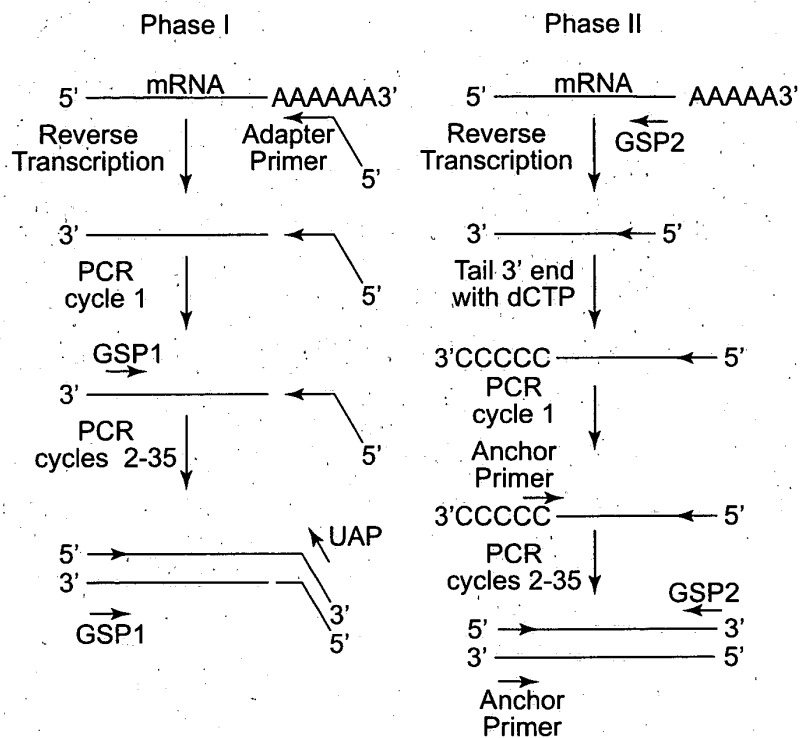


Fig. 4

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Nucleotide Identity

TRI	82.8	49.0	43.7	52.3	51.0	52.0	51.5	51.1	52.8	54.5
84.1	TRI	48.2	39.1	44.9	50.0	50.0	49.5	48.0	49.8	52.5
45.5	43.9	TRI	58.1	77.0	67.7	68.9	67.9	69.4	69.4	72.5
35.6	35.6	52.3	AFI	60.1	58.8	55.1	53.8	55.3	56.8	56.8
44.7	40.9	73.5	52.3	CFI	65.7	68.7	67.7	68.4	67.7	72.2
47.7	44.7	70.5	49.2	64.4	TRI	75.0	74.5	62.6	75.5	78.3
42.4	38.6	66.7	46.2	63.6	78.8	C	84.1	84.3	84.3	84.3
42.4	38.6	65.2	45.5	62.9	78.0	87.9	R	92.4	91.2	92.2
42.4	38.6	66.7	46.2	63.6	78.8	88.6	97.0	B	94.4	95.5
42.4	38.6	64.4	46.2	62.9	78.8	90.9	96.2	98.5	M	98.7
45.5	42.4	73.5	47.7	68.2	87.1	91.7	97.7	98.5	100	H

Amino Acid Identity

Fig. 5

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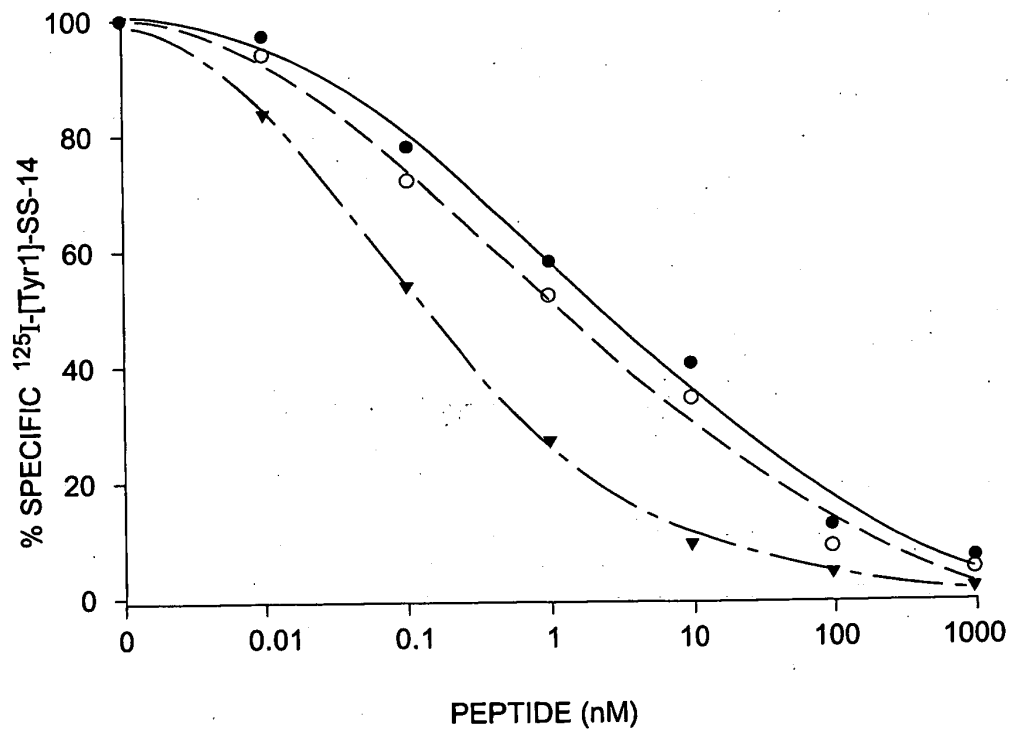
THE INFORMATION

Comparison of Amino Acid Sequences of Peptides Derived from Preprosomatostatin Ia

	-20	-10	+1	+10	+14	
Rainbow trout ^b						SEQ ID NO: 4
Hagfish ^d						SEQ ID NO: 27
Lamprey ^d						SEQ ID NO: 1
Torpedod						SEQ ID NO: 1
Ratfish ^d						SEQ ID NO: 28
Bowfin ^d						SEQ ID NO: 29
Sturgeon ^d						SEQ ID NO: 30
Carfish ^d						SEQ ID NO: 1
Salmon ^d						SEQ ID NO: 1
Anglerfish ^c						SEQ ID NO: 31
Eel ^d						SEQ ID NO: 1
Flounder ^d						SEQ ID NO: 2
Sculpin ^d						SEQ ID NO: 2
Frog ^c						SEQ ID NO: 1
Salamander ^d						SEQ ID NO: 1
Alligator ^d						SEQ ID NO: 1
Pigeon ^d						SEQ ID NO: 1
Ovine ^d						SEQ ID NO: 32

Fig. 6

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*Fig. 8*